

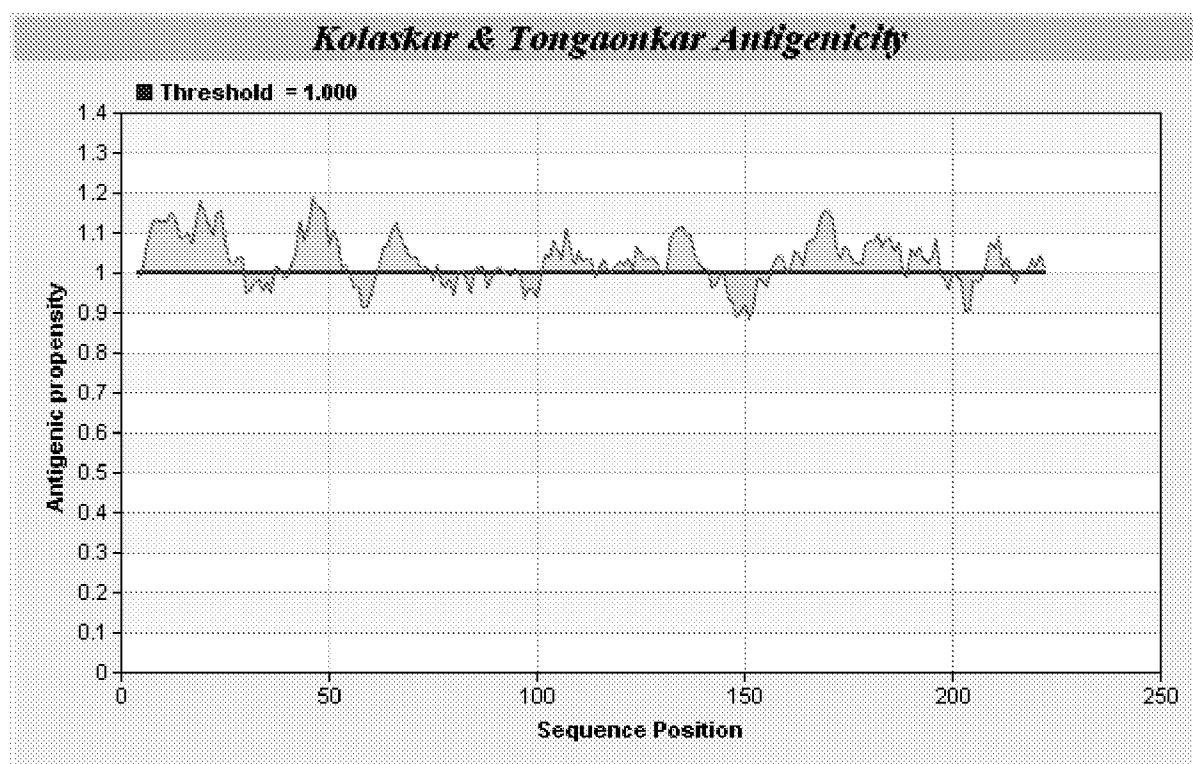
IEDB Analysis Resource

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Kolaskar & Tongaonkar Antigenicity

Sequence:

```
1 MTFFKPSTVV LTASALALSG CVADPVTGQQ SPNKSAMYGL GGAAVCGIVG ALTHSGKGAR
61 NSALACGAIG AGVGGYMDYQ EQRLRQNLAG TQIEIQRQGN QIRLVMPESV TFATGSAALG
121 GSAQYALNTA AQTLVQYPDT TLTINGHTDN TGSDAVNNPL SQHRAQAVAY YLQTRGVAAS
181 RLTVYGYGSH MPVASNATVE GRAQNRNRVEI LINPDQRAVN AARHM
```

Center position: 4 Window size: 7**Average: 1.032 Minimum: 0.887 Maximum: 1.190 Threshold: 1.000**[Click here to view plotted values in table format](#)

Predicted peptides:

No.	Start Position	End Position	Peptide	Peptide Length
1	5	29	KPSTVVLTASALALSGCVADPVTGQ	25
2	41	54	GGAAVCGIVGALTH	14

3	62	74	SALACGAIGAGVG	13
4	102	113	IRLVMPESVTFA	12
5	115	129	GSAALGGSAQYALNT	15
6	132	141	QTLVQYPDTT	10
7	161	188	SQHRAQAVAYYLQTRGVAASRLTVYGYG	28
8	190	197	HMPVASNA	8
9	208	213	VEILIN	6

Reference: Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. FEBS Lett. 1990 Dec 10;276(1-2):172-4.

Scale values: A:1.064, C:1.412, D:0.866, E:0.851, F:1.091, G:0.874, H:1.105, I:1.152, K:0.93, L:1.25, M:0.826, N:0.776, P:1.064, Q:1.015, R:0.873, S:1.012, T:0.909, V:1.383, W:0.893, Y:1.161